

OIIPE

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,035

DATE: 05/29/2001 JAN 23 2001

TIME: 13:00:18

TECH CENTER 1600/2900

Input Set : A:\227274078.ST25.txt

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3 <110> APPLICANT: Lang, Jas  
 5 <120> TITLE OF INVENTION: Detecting the Expression of the DESC1 Gene in Squamous Cell Carcinoma

7 <130> FILE REFERENCE: 22727/04078  
 9 <140> CURRENT APPLICATION NUMBER: 09/674,035  
 10 <141> CURRENT FILING DATE: 1999-11-11  
 12 <150> PRIOR APPLICATION NUMBER: PCT/IB99/01818  
 13 <151> PRIOR FILING DATE: 1999-11-11  
 15 <160> NUMBER OF SEQ ID NOS: 10  
 17 <170> SOFTWARE: PatentIn version 3.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1269  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (1)..(1269)  
 28 <400> SEQUENCE: 1

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33	ccc tgg gtt atc ggc ctc gtc atc ttc ata tcc ctg att gtc ctg gca	96
34	Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala	
35	20 25 30	
37	gtg tgc att gga ctc act gtt cat tat gtg aga tat aat caa aag aag	144
38	Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys	
39	35 40 45	
41	acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat	192
42	Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr	
43	50 55 60	
45	gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag	240
46	Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln	
47	65 70 75 80	
49	aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg	288
50	Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg	
51	85 90 95	
53	gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa gac aag cat	336
54	Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Asp Lys His	
55	100 105 110	
57	gga gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag	384
58	Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu	
59	115 120 125	
61	gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag	432
62	Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys	
63	130 135 140	
65	ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa	480
66	Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys	
67	145 150 155 160	

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71					165					170					175		
73	tgc	gga	aca	cga	aga	agt	aaa	act	cta	ggt	cag	agt	ctc	agg	atc	gtt	576
74	Cys	Gly	Thr	Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	
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77	ggt	ggg	aca	gaa	gta	gaa	gag	ggt	gaa	tgg	ccc	tgg	cag	gct	agc	ctg	624
78	Gly	Gly	Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	
79			195					200					205				
81	cag	tgg	gat	ggg	agt	cat	gcg	tgt	gga	gca	acc	tta	att	aat	gcc	aca	672
82	Gln	Trp	Asp	Gly	Ser	His	Ala	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	
83		210					215					220					
85	tgg	ctt	gtg	agt	gct	gct	cac	tgt	ttt	aca	aca	tat	aag	aac	cct	gcc	720
86	Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	Ala	
87	225					230				235					240		
89	aga	tgg	act	gct	tcc	ttt	gga	gta	aca	ata	aaa	cct	tcg	aaa	atg	aaa	768
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94	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	His	Pro	Ser	
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97	cat	gac	tat	gat	att	tct	ctt	gca	gag	ctt	tct	agc	cct	gtt	ccc	tac	864
98	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	Pro	Val	Pro	Tyr	
99		275					280					285					
101	aca	aat	gca	gta	cat	aga	gtt	tgt	ctc	cct	gat	gca	tcc	tat	gag	ttt	912
102	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	Ala	Ser	Tyr	Glu	Phe	
103		290					295					300					
105	caa	cca	ggt	gat	gtg	atg	ttt	gtg	aca	gga	ttt	gga	gca	ctg	aaa	aat	960
106	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	Phe	Gly	Ala	Leu	Lys	Asn	
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109	gat	ggt	tac	agt	caa	aat	cat	ctt	cga	caa	gca	cag	gtg	act	ctc	ata	1008
110	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	Gln	Ala	Gln	Val	Thr	Leu	Ile	
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113	gac	gct	aca	act	tgc	aat	gaa	cct	caa	gct	tac	aat	gac	gcc	ata	act	1056
114	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	
115			340						345				350				
117	cct	aga	atc	tta	tgt	gct	ggc	tcc	tta	gaa	gga	aaa	aca	gat	gca	tgc	1104
118	Pro	Arg	Ile	Leu	Cys	Ala	Gly	Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	
119		355					360					365					
121	cag	ggt	gac	tct	gga	gga	cca	ctg	gtt	agt	tca	gat	gct	aga	gat	atc	1152
122	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	
123		370					375					380					
125	tgg	tac	ctt	gct	gga	ata	gtg	agc	tgg	gga	gat	gaa	tgt	gcg	aaa	ccc	1200
126	Trp	Tyr	Leu	Ala	Gly	Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	
127	385				390				395				400				
129	aac	aag	cct	ggt	gtt	tat	act	aga	gtt	acg	gcc	ttg	cgg	gac	tgg	att	1248
130	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	
131				405					410				415				
133	act	tca	aaa	act	ggt	atc	taa										1269

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138 <210> SEQ ID NO: 2
139 <211> LENGTH: 422
140 <212> TYPE: PRT
141 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 2
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150                               20                               25                               30
153 Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
154                               35                               40                               45
157 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
158                               50                               55                               60
161 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
162 65                               70                               75                               80
165 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
166                               85                               90                               95
169 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Asp Lys His
170                               100                              105                              110
173 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
174                               115                              120                              125
177 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
178                               130                              135                              140
181 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
182 145                              150                              155                              160
185 Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
186                               165                               170                               175
189 Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
190                               180                               185                               190
193 Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
194                               195                               200                               205
197 Gln Trp Asp Gly Ser His Ala Cys Gly Ala Thr Leu Ile Asn Ala Thr
198                               210                               215                               220
201 Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
202 225                              230                              235                              240
205 Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
206                               245                               250                               255
209 Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
210                               260                               265                               270
213 His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
214                               275                               280                               285
217 Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
218                               290                               295                               300
221 Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
222 305                              310                              315                              320
225 Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
226                               325                               330                               335

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233 Pro Arg Ile Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
234          355          360          365
237 Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
238          370          375          380
241 Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
242 385          390          395          400
245 Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
246          405          410          415
249 Thr Ser Lys Thr Gly Ile
250          420
253 <210> SEQ ID NO: 3
254 <211> LENGTH: 1269
255 <212> TYPE: DNA
256 <213> ORGANISM: Homo sapiens
258 <220> FEATURE:
259 <221> NAME/KEY: CDS
260 <222> LOCATION: (1)..(1269)
262 <400> SEQUENCE: 3
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264 Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
265 1          5          10          15
267 ccc tgg gtt atc ggc ctc gtc atg ttc ata tcc ctg att gtc ctg gca      96
268 Pro Trp Val Ile Gly Leu Val Met Phe Ile Ser Leu Ile Val Leu Ala
269          20          25          30
271 gtg tgc att gga gtc act gtt cat tat gtg aga tat aat caa aag aag      144
272 Val Cys Ile Gly Val Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
273          35          40          45
275 acc tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat      192
276 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
277          50          55          60
279 gct gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag      240
280 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
281 65          70          75          80
283 aga ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg      288
284 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
285          85          90          95
287 gaa gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat      336
288 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
289          100          105          110
291 gga gtg ttg gct cat atg ctg ttg att tct aga ttt cac tct act gag      384
292 Gly Val Leu Ala His Met Leu Leu Ile Ser Arg Phe His Ser Thr Glu
293          115          120          125
295 gat cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag      432
296 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
297          130          135          140
299 ctg caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa      480
300 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys

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301	145				150				155				160				
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308	Cys	Gly	Thr	Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	
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312	Gly	Gly	Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	
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315	cag	tgg	gat	ggg	agt	cat	cgc	tgt	gga	gca	acc	tta	att	aac	gcc	aca	672
316	Gln	Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	
317		210				215					220						
319	tgg	ctt	gtg	agt	gct	gct	cac	tgt	ttt	aca	aca	tat	aag	aac	cct	gcc	720
320	Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	Ala	
321	225				230				235					240			
323	aga	tgg	act	gct	tcc	ttt	gga	gta	aca	ata	aaa	cct	tcg	aaa	atg	aaa	768
324	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	Met	Lys	
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327	cgg	ggt	ctc	cgg	aga	ata	att	gtc	cat	gaa	aaa	tac	aaa	cac	cca	tca	816
328	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	His	Pro	Ser	
329			260					265			270						
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336	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	Ala	Ser	Tyr	Glu	Phe	
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348	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	
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351	cct	aga	atg	tta	tgt	gct	ggc	tcc	tta	gaa	gga	aaa	aca	gat	gca	tgc	1104
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363	aac	aag	cct	ggt	gtt	tat	act	aga	gtt	acg	gcc	ttg	cgg	gac	tgg	att	1248
364	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	
365				405				410			415						

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